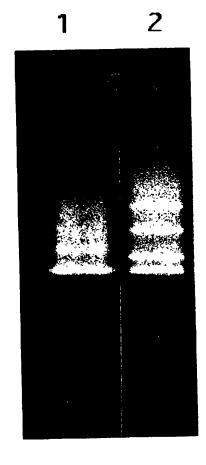
Fig. 1

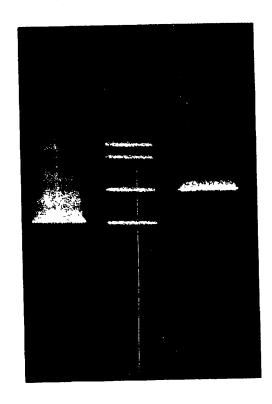


: Wild Type

Heterozygote Mutant

Fig. 2

3 2

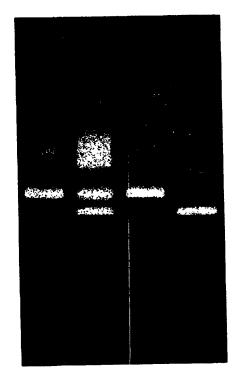


1: Wild Type

2: Heterozygote Mutant

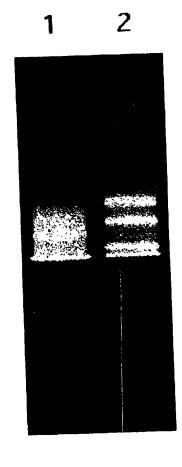
3: Homozygote Mutant

Fig. 3



- 1,3:Wild Type
- 2: Heterozygote Mutant
- 4: Homozygote Mutant

Fig. 4



1: Wild Type

 $2: \frac{\mathsf{Heterozygote}}{\mathsf{Mutant}}$

Fig. 5

2



1:Wild Type

2 : Heterozygote Mutant

Fig. 6

Thr Gln Thr Val Pro

C 350 ACT CAG AC / GTA CCT

Maddall

Fig. 7

Arg ValGln / AspMet Trp

GTC CAG / GG GAC ATG

Mulman

Fig. 8

ValGlnTrpAspMet

GTC CAG TGG GAC ATG

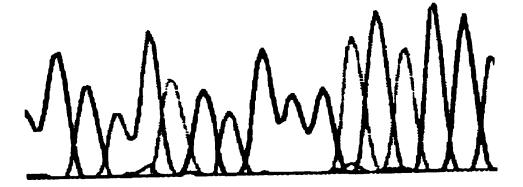


Fig. 9

Cys Ile Asn Tyr

Å
ttag AA AT/ AAC TAT
C

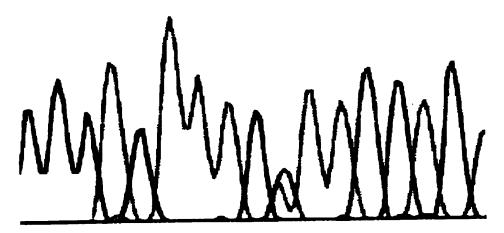


Fig. 10

Cys Ile Asn Tyr

495
ttag AA ATC AAC TAT

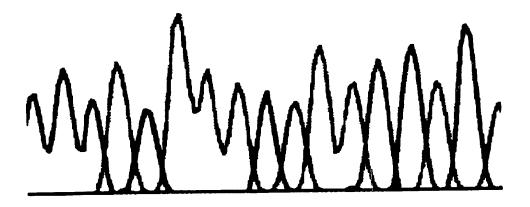


Fig. 11

264

Ser LeuGlu / IleIle Leu

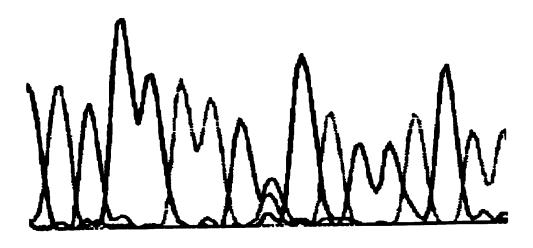
791

785

790**C**

795

CTG GAA T/G ATT ATA T



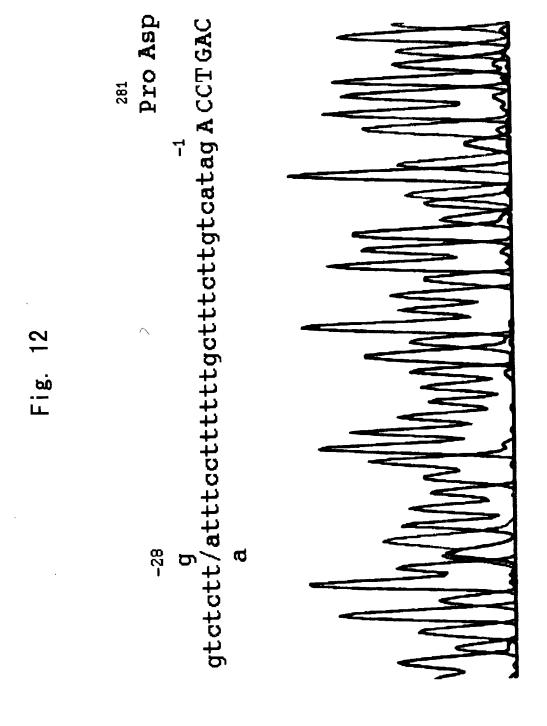
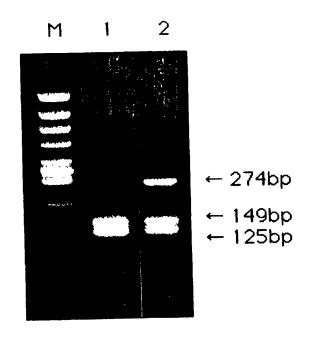


Fig. 13



- M: Molecular Weight Marker
 - 1: Wild Type
- 2: Heterozygote Mutant
- 3: Homozygote Mutant

Fig. 14



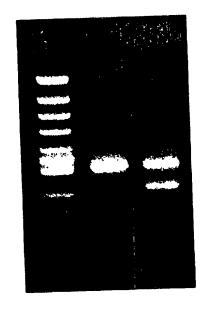
M: Molecular Weight Marker

1: Wild Type

2: Heterozygote Mutant

Fig. 15

2 Μ 1



- ← 297bp
- ← 220bp
- ← 77bp
- Molecular M:Weight Marker
- 1: Wild Type
- 2: Heterozygote Mutant